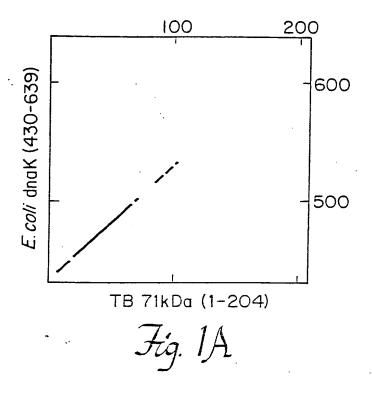
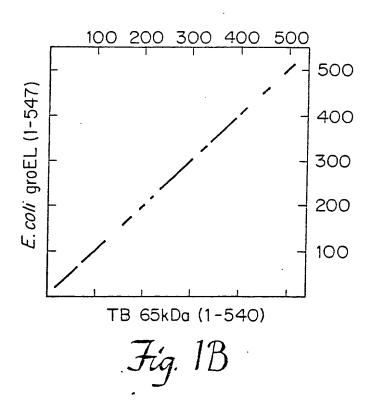
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Tip Stress Proteins and Uses Therefor Information Richard A. Young, et al.





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	 i ~	10	20	30	40	50	09	. 70
	MLRLP!	TVFRQMRPV	SRVLAPHLTI	AYAKDVKFG.	ADARALMLOG	' VDLLADAVA	MLRLPTVFRQMRPVSRVLAPHLTRAYAKDVKFGADARALMLOGVDLLADAVAVTMGPKGRTVTTFOGWGG	, SOMBORT I
	1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	: MA	AKDVKFG	::: ::: NDARVKMLRG	: ::: VNVLADAVK	AKDVKFGNDARVKMLRGVNVLADAVKVTLGPKGRNVVLDKSFGA	VLDKSFGA
7	71	80	06	100	110	120	130	140
	PKVTKI : ::: PTITKE	GOTVAKSI:::::	DLKDKYKNIC :: :: EPEDKFENMG	SAKLVQDVANI : :: :AQMVKEVASI	VTNEEAGDGT' : :::: (ANDAAGDGT'	, TTATVLARS :::::: TTATVLAOA	PKVTKDGVTVAKSIDLKDKYKNIGAKLVQDVANNTNEEAGDGTTTATVLARSIAKEGFEKISKGANPVEI : :::::::::::::::::::::::::::::::::::	KGANPVEI::::
141	11	150	160	170	180	190	. 200	210
	RRGVMI:: KRGIDK	AVDAVIAE) :::: AVTAAVEEI	LKKQSKPVTT :: :: LKALSVPCSD	PEEIAQVATI :::::: SKAIAQVGTI	SANGDKEIGH	NIISDAMKK : ::: KLIAEAMDK	RRGVMLAVDAVIAELKKQSKPVTTPEEIAQVATISANGDKEIGNIISDAMKKVGRKGVITVKDGKTLNDE :: : : : : : : : : : : : : : : : : : :	GKTLNDE:
211		220	230	240	250	260	270	280
	LEIIEGMKFDR : ::: ::: LDVVEGMQFDR	MKFDRGYIE : ::::: MQFDRGYLS	SPYFINTSKG ::::: SPYFINKPET	QKCEFQDAYV : GAVELESPFI	TLESEKKISSI:::::::::::::::::::::::::::::::	' [QSIVPALE::: REMLPVLE!	GYISPYFINTSKGOKCEFQDAYVLLSEKKISSIQSIVPALEIANAHRKPLVIIAEDVDG ::::::: GYLSPYFINKPETGAVELESPFILLADKKISNIREMLPVLEAVAKAGKPLLIIAEDVEG	IAEDVDG:::::::
281		290	300	310	320	330	340	350
	EALSTL:	VLNRLKVGL : : VVNTIRGIV	QVVAVKAPGI : ::::: 'KVAAVKAPGI	FGDNRKNQLK :::::::	, DMAIATGGAV : ::: :: DIATLTGGTV	'FGEEGLTLN :: ISEE-IGME	EALSTLVLNRLKVGLQVVAVKAPGFGDNRKNQLKDMAIATGGAVFGEEGLTLNLEDVQPHDLGKVGEVIV :::::::::::::::::::::::::::::::::::	KVGEVIV :
351		360	370	380	390	400	410	420
	rkddami::	LLKGKGDKA	QIEKRIQEII	LEQLDVTTSE	YEKEKLNERL	AKLSDGVAV	TKDDAMLLKGKGDKAQIEKRIQEIIEQLDVTTSEYEKEKLNERLAKLSDGVAVLKVGGTSDVEVNEKKDR	, VNEKKDR
4	VKDTTT.	IIDGVGEEA	AIQGRVAQII	ROQIEEATSD	YDREKLQERV	AKLAGGVAV	NKDTTTIIDGVGEEAAIQGRVAQIRQQIEEATSDYDREKLQERVAKLAGGVAVIKVGAATEVEMKEKKAR	:::: MKEKKAR

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	421	430	440 4	450	460	470	480	490
HUMP1	VTDALN	ATRAAVEEGI	VTDALNATRAAVEEGIVLGGGCALLRCIPALDSLTPANEDQKIGIEIIKRTLKIPAMTIAKNAGVEGSLI	PALDSLTP!	ANEDQKIGI	EIIKRTLE	KIPAMTIA	KNAGVEGSLI
GROEL	: ::: :::: VEDALHATRA	ATRAAVEEGU	: ::: ::::::::::::::::::::::::::::::::	: SKLADLRGÇ	:::: SQNEDQNVVS	; SSL-RAME	: Saperqivi	: : : : LNCGEEPSVV
	491	500	510 5	520	530	540	550	560
HUMP1	VEKIMQ	SSSEVGYDAM	VEKIMQSSSEVGYDAMAGDFVNMVEKGIIDPTKVVRTALLDAAGVASLLTTAEVVVTEIPKEEKDPGMGA	IDPTKVVR	TALLDAAGV	ASLLTTA	SVVVTEIPI	KEEKDPGMGA
GROEL	ANTVKG	GDGNYGYNAA	ANTVKGGDGNYGYNAATEEYGNMIDMGILDPTKVTRSALQYAASVAGLMITTECMVTDLPKND-AADLGA	LDPTKVTRS	SALQYAASV	:: :: : : : : : : : : : : : : : : : :	SCMVTDLP	KND-AADLGA
	561	570						
HUMP1	MGGMGG	MGGMGGGMGGGMF						
	••							
GROEL	AGGMGG	А ССМССМССММ—				•		
Total	score = 4667,		5 breaks tof EAE norrible matcher between regidner		100			
2	ז מ כוו כד כד כ		מימימים לי	וומרכווכא	מבראבביוו ד			
rand	25 random runs Aliqnment score	= 65.34 SD		Standard deviation	tion =	18.94	Mean =	3429.48

OUT 2 8 YOUR WEEK

, M M	, MLRLPT : M	LVERQMRP	ZU , VSRVLAPHL	10 20 30 40 50 60 70 , , , , , , , , , , , , , , , , , , ,	40 , ADARALMLQGV ::::::	50 , /DLLADAVA' :::: .NSLADAVK'	30 40 50 60 70 , YAKDVKFGADARALMLQGVDLLADAVAVTMGPKGRTVIIEQSWGS :: ::::::::::::::::::::::::::::::::::	70 IEQSWGS : :: LEKKWGA
1 PKVTKD:::	⊣ ••	80 COUTVAKS	90 IDLKDKYKN : : : : IELEDPYEK	1 80 90 100 110 120 130 140 ,	110 / NTNEEAGDGT1 : ::::	120 , ' :::::::::::::::::::::::::::::::::::	120 130 140 ' 'TTATVLARSIAKEGFEKISKGANPVEI::::::::::::::::::::::::::::::::::::	140 GANPVEI :::: GANPLGL
(GV)	Σ FI Σ X	150 SAVDAVIA	160 ELKKQSKPV' : : : : TLLKDAKEVJ	1 150 160 170 180 190 200 210, RRGVMLAVDAVIAELKKQSKPVTTPEEIAQVATISANGDKEIGNIISDAMKKVGRKGVITVKDGKTLNDE :: :: : : : : : : : : : : : : : : : :	180 ' SANGDKEIGN :: :: ::	190 '' IIISDAMKKY : ::::	200 VGRKGVITVKD	210 GRTLNDE :
1 LEIIEG :: :: LELTEG	Б Н П	220 MKFDRGY : :: ::	230 ISPYFINTSI :: :: ISGYFVTDAL	230 240 250 260 270 280 , , , , , , , , , , , , , , , , , , ,	250 , 7LLSEKKISSI :: : :	260 , QSIVPALE: :::	270 IANAHRKPLVI : : :	280 ' IAEDVDG ::::::
1.5 1.5 1.5	1 EALSTE ::::::	290 ,VLNRLKV(::::,VLNKIRG:	300 , GLQVVAVKAH ::::::	1 290 300 310 320 330 340 350, 36, 20, 37, 20, 350, 36, 36, 36, 36, 36, 36, 36, 36, 36, 36	320 DMAIATGGAV :::::::	330 , FGEEGLTLN :::	340 VLEDVQPHDLGI :: ::	350 KVGEVIV : :
		360	370	380	390	400	410	420
TKDDAMI ::: TKDETTI	AM	ILLKGKGD! : :: 'IVEGAGD'	KAQIEKRIQE : : FDAIAGRVAÇ	LLKGKGDKAQIEKRIQEIIEQLDVTTSEYEKEKLNERLAKLSDGVAVLKVGGTSDVEVNEKKDR : :: : : : : : : : : : : : : : : : : :	YEKEKLNERL : ::::::	AKLSDGVAV::::	/LKVGGTSDVE/ : : : : : : / /IKAGAATEVE!	NEKKDR:::

App No.: Stress Proteins and Uses Therefor

Richard A. Young, et al.

490 IEDAVRNAKAAVEEGIVAGGGVTLLQAAPALDKLKLTGDEAT-GANIVKVALEAPLKQIAFNSGMEPGVV 560 VTDALNATRAAVEEGIVLGGGCALLRCIPALDSLTPANEDQKIGIEIIKRTLKIPAMTIAKNAGVEGSLI VEKIMQSSSEVGYDAMAGDFVNMVEKGIIDPTKVVRTALLDAAGVASLLTTAEVVVTEIPKEEKDPGMGA AEKVRNLSVGHGLNAATGEYEDLLKAGVADPVKVTRSALQNAASIAGLFTT-EAVVADKPEKTAAPASDP Mean = 3413.16550 255 identities out of 540 possible matches between residues 470 540 23.86 Standard deviation = 460 530 450 440 510 47.73 SD 7 breaks MGGMGGGMF TGGMGG-MD---F score = 4552, Alignment score 25 random runs 491 HUMPI ML65K HUMP1 ML65K Total ML65K HUMP1

430

421

App No.:

MLRLPTVFRQMRPVSRVLAPHLTRAYAKDVKFGADARALMLQGVDLLADAVAVTMGPKGRTVI I EQSWGS

TB65K

HUMP1

9

50

30

20

--AKTIAYDEEARRGLERGLNALADAVKVTLGPKGRNVVLEKKWGA

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140 210 280 PTITNDGVSIAKEIELEDPYEKIGAELVKEVAKKTDDVAGDGTTTATVLAQALRKEGLRNVAAGANPLGL RRGVMLAVDAVIAELKKQSKPVTTPEEIAQVATISANGDKEIGNIISDAMKKVGRKGVITVKDGKTLNDE KRGIEKAVEKVTETĻLKGAKEVETKEQIAATAAISA-GDQSIGDLIAEAMDKVGNEGVITVEESNTFGLQ LEIIEGMKFDRGYISPYFINTSKGQKCEFQDAYVLLSEKKISSIQSIVPALEIANAHRKPLVIIAEDVDG LELTEGMRFDKGYISGYFVTDPERQEAVLEDPYILLVSSKVSTVKDLLPLLEKVIGAGKPLLIIAEDVEG 350 420 PKVTKDGVTVAKSIDLKDKYKNIGAKLVQDVANNTNEEAGDGTTTATVLARSIAKEGFEKISKGANPVEI TKDDAMLLKGKGDKAQIEKRIQEIIEQLDVTTSEYEKEKLNERLAKLSDGVAVLKVGGTSDVEVNEKKDR TKDETTIVEGAGDTDA I AGRVAQ I RQE I ENSDSDYDREKLQERLAKLAGGVAV I KAGAATEVELKERKHR EALSTLVLNRLKVGLQVVAVKAPGFGDNRKNQLKDMAIATGGAVFGEEGLTLNLEDVQPHDLGKVGEVIV EALSTLVVNKIRGTFKSVAVKAPGFGDRRKAMLQDMAILTGGQVISEE-VGLTLENADLSLLGKARKVVV 130 200 120 190 260 ••• 400 330 110 180 250 320 390 100 170 310 380 90 160 230 300 370 80 150 290 360 141 351 TB65K **TB65K** HUMP1 HUMP1 HUMP1 rB65K TB65K TB65K HUMP1 HUMP1

App No.: 10/046,649 10046649 .102802

Mean = 3413.16

23.23

Standard deviation =

SD

Alignment score = 25 random runs

identities out of 540 possible matches between residues

score = 4560, 5 breaks

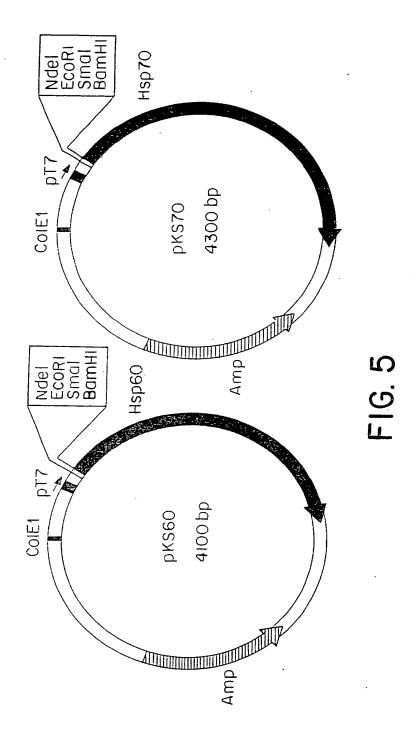
Total 257

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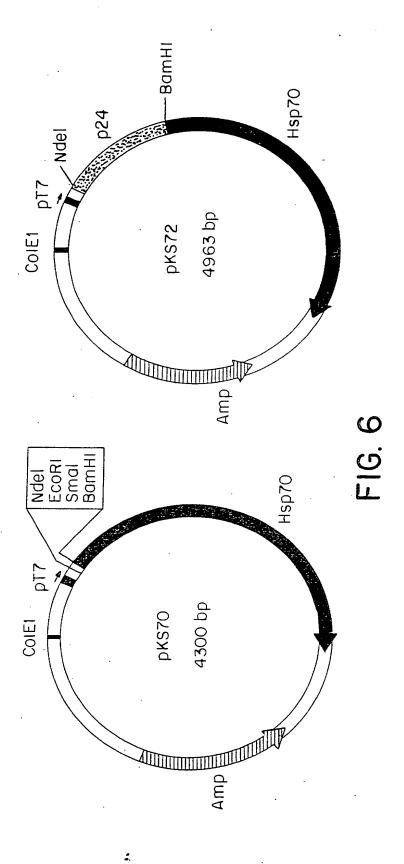
490 560 VTDALNATRAAVEEGIVLGGGCALLRCIPALDSLTPANEDQKIGIEIIKRTLKIPAMTIAKNAGVEGSLI IEDAVRNAKAAVEEGIVAGGGVTLLQAAPTLDELK-LEGDEATGANIVKVALEAPLKQIAFNSGLEPGVV VEKIMQSSSEVGYDAMAGDFVNMVEKGIIDPTKVVRTALLDAAGVASLLTTAEVVVTEIPKEEKDPGMGA AEKVRNLPAGHGLNAQTGVYEDLLAAGVADPVKVTRSALQNAASIAGLFLTTEAVVADKPEKEKASVPG-480 550 470 540 460 530 450 520 510 MGGMGGGMGGGMF ---GGDMGGMDF 430 500 421 561 491 TB65K **TB65K** HUMP1 , HUMP1 **HUMP1** TB65K

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